

SEQUENCE LISTING

<110> Boehringer Ingelheim Pharma KG

<120> Method for identifying substances which positively influence inflammatory conditions

<130> 1/1179

<140>

<141>

<150> US 60/257,856

<151> 2000-12-22

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 1

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ttt                                             63
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<210> 2

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 2

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gtcgtcaaga  tgctaccggt  cagga                                             25
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<210> 3

<211> 802

<212> DNA

<213> Homo sapiens

<400> 3

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tatatggaat  ggatcctgaa  ctccttagca  tggtagcaag  accagtctgt  gcagtcttac  180
ttctctttcc  tattacagaa  aagtatgaag  tattcagaac  agaagaggaa  gaaaaaataa  240
aatctcaggg  acaagatggt  acatcatcag  tatatttcat  gaagcaaaca  atcagcaatg  300
cctgtggaac  aattggactg  attcatgcta  ttgcaaacaa  taaagacaag  atgcactttg  360
aatctggatc  aaccttgaaa  aaattcctgg  aggaatctgt  gtcaatgagc  cctgaagaac  420
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gagccagata cctggagaac tatgatgcca tccgagttac tcatgagacc agtgcccatg 480
aaggtcagac tgaggcacca agtatagatg agaaagtaga tcttcatttt attgcattag 540
ttcatgtaga tgggcatctc tatgaattag atgggcggaa gccatttcca attaaccatg 600
gtgaaactag tgatgaaact ttattagagg atgccataga agtttgcaag aagtttatgg 660
agcgcgaccc tgatgaacta agatttaatg cgattgctct ttctgcagca tagcttgtca 720
ataatggaaa caccaaaaac tgtattattt gcaactaaat tttctctgcc catacactaa 780
ctcaaaaatt ttgatatttt cc 802

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<210> 4
<211> 230
<212> PRT
<213> Homo sapiens

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<400> 4
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Asn Gln Phe Leu Lys Gln Leu Gly Leu His Pro Asn Trp Gln Phe Val
      20              25              30
Asp Val Tyr Gly Met Asp Pro Glu Leu Leu Ser Met Val Pro Arg Pro
      35              40              45
Val Cys Ala Val Leu Leu Leu Phe Pro Ile Thr Glu Lys Tyr Glu Val
      50              55              60
Phe Arg Thr Glu Glu Glu Glu Lys Ile Lys Ser Gln Gly Gln Asp Val
      65              70              75              80
Thr Ser Ser Val Tyr Phe Met Lys Gln Thr Ile Ser Asn Ala Cys Gly
      85              90              95
Thr Ile Gly Leu Ile His Ala Ile Ala Asn Asn Lys Asp Lys Met His
      100             105             110
Phe Glu Ser Gly Ser Thr Leu Lys Lys Phe Leu Glu Glu Ser Val Ser
      115             120             125
Met Ser Pro Glu Glu Arg Ala Arg Tyr Leu Glu Asn Tyr Asp Ala Ile
      130             135             140
Arg Val Thr His Glu Thr Ser Ala His Glu Gly Gln Thr Glu Ala Pro
      145             150             155             160
Ser Ile Asp Glu Lys Val Asp Leu His Phe Ile Ala Leu Val His Val
      165             170             175
Asp Gly His Leu Tyr Glu Leu Asp Gly Arg Lys Pro Phe Pro Ile Asn
      180             185             190
His Gly Glu Thr Ser Asp Glu Thr Leu Leu Glu Asp Ala Ile Glu Val
      195             200             205
Cys Lys Lys Phe Met Glu Arg Asp Pro Asp Glu Leu Arg Phe Asn Ala
      210             215             220

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Ile Ala Leu Ser Ala Ala
225 230

<210> 5
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
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<210> 6
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
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<210> 7
<211> 866
<212> DNA
<213> Homo sapiens

<400> 7
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gcaaagtgtg tggattagc aactgagaaa aaacagaaat ccattctgta tgatgagcga 180
agtgtacaca aagtagaacc aattaccaag catatagggt tgggtgtacag tggcatgggc 240
cccgattaca gagtgcctgt gcacagagct cgaaaactag ctcaacaata ctatcttgtg 300
taccaagaac ccattcctac agctcagctg gtacagagag tagcttctgt gatgcaagaa 360
tatactcagt cagggtggtg tcgtccattt ggagtttctt tacttatttg tggttggaat 420
gagggacgac catattttatt tcagtcagat ccactctggag cttacttttg ctggaaaagct 480
acagcaatgg gaaagaacta tgtgaatggg aagactttcc ttgagaaaag atataatgaa 540
gatctggaac ttgaagatgc cattcataca gccatcttaa ccctaaagga aagctttgaa 600
gggcaaataa cagaggataa catagaagtt ggaatctgca atgaagctgg atttaggagg 660
cttactccaa ctgaagttaa ggattacttg gctgccatag cataacaatg aagtgactga 720
aaaatccaga atttcagata atctatctac ttaaacaatg ttaaagtatg ttttgttttg 780
cagacttttt gcatacttat ttctacatgg tttaaatcga ctgtttttta aatgacactt 840
ataaatccta ataaactgtt aaaccc 866

<210> 8
<211> 234
<212> PRT
<213> Homo sapiens

<400> 8

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Ala	Pro	Ser 35	Val	Gly	Ile	Lys	Ala 40	Ala	Asn	Gly	Val	Val 45	Leu	Ala	Thr
Glu	Lys 50	Lys	Gln	Lys	Ser	Ile 55	Leu	Tyr	Asp	Glu	Arg 60	Ser	Val	His	Lys
Val 65	Glu	Pro	Ile	Thr	Lys 70	His	Ile	Gly	Leu	Val 75	Tyr	Ser	Gly	Met	Gly 80
Pro	Asp	Tyr	Arg 85	Val	Leu	Val	His	Arg	Ala 90	Arg	Lys	Leu	Ala	Gln 95	Gln
Tyr	Tyr	Leu	Val 100	Tyr	Gln	Glu	Pro	Ile 105	Pro	Thr	Ala	Gln	Leu 110	Val	Gln
Arg	Val 115	Ala	Ser	Val	Met	Gln	Glu 120	Tyr	Thr	Gln	Ser	Gly 125	Gly	Val	Arg
Pro	Phe 130	Gly	Val	Ser	Leu	Leu 135	Ile	Cys	Gly	Trp	Asn 140	Glu	Gly	Arg	Pro
Tyr 145	Leu	Phe	Gln	Ser 150	Asp	Pro	Ser	Gly	Ala 155	Tyr	Phe	Ala	Trp	Lys	Ala 160
Thr	Ala	Met	Gly	Lys 165	Asn	Tyr	Val	Asn	Gly 170	Lys	Thr	Phe	Leu	Glu 175	Lys
Arg	Tyr	Asn	Glu 180	Asp	Leu	Glu	Leu	Glu 185	Asp	Ala	Ile	His	Thr 190	Ala	Ile
Leu	Thr 195	Leu	Lys	Glu	Ser	Phe	Glu 200	Gly	Gln	Met	Thr	Glu 205	Asp	Asn	Ile
Glu 210	Val	Gly	Ile	Cys	Asn	Glu 215	Ala	Gly	Phe	Arg	Arg 220	Leu	Thr	Pro	Thr
Glu 225	Val	Lys	Asp	Tyr 230	Leu	Ala	Ala	Ile	Ala						